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Attorney Docket No. 15966-581 CIP
(Cura-81 CIP)



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS: Kerry E. Quinn et al.
SERIAL NUMBER: 09/996,015 EXAMINER: Not yet assigned
FILING DATE: November 28, 2001 ART UNIT: Not yet assigned
FOR: AORTIC CARBOXYPEPTIDASE-LIKE PROTEINS AND NUCLEIC ACIDS
ENCODING SAME

Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Prior to examination of the above-identified application, please amend the application as set forth below and consider the following remarks:

In the Specification:

Replace the first full paragraph on page 6:

“FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) and the ACPL1a polypeptide (SEQ ID NO:2) (ALO35460_GENESCAN_predicted_pep”).”

with the following re-written paragraph:

-- FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO:13) and the ACPL1a polypeptide (SEQ ID NO:2) (ALO35460_GENESCAN_predicted_pep”).--

A marked-up version showing changes made to the specification is submitted herewith as **Appendix A**, pursuant to 37 C.F.R. § 1.121(b)(1)(iii).

Please insert the sequence listing, pages 1-51, at the end of the specification.

In the Drawings:

Pursuant to 37 C.F.R. § 1.121(d), Applicants submit herewith, in **Appendix B**, separate sheets of drawings showing proposed changes in red. Specifically, Applicants wish to cancel Figure 2 of the present application and insert new Figure 2. Applicants further wish to amend Figures 14, 15, and 16. Applicants respectfully request Examiner's approval of these changes.

Applicants additionally submit herewith, in **Appendix C**, drawings in compliance with 37 C.F.R. § 1.84, incorporating the above changes.

REMARKS

In response to the Notice to File Missing Parts of Nonprovisional Application, Applicants submit herein an initial computer readable form (CRF) copy of the "Sequence Listing," and an initial paper copy of the "Sequence Listing." No new matter has been added. A statement that the content of the paper and computer readable copies are the same and include no new matter, in compliance with 37 C.F.R. §§ 1.821 – 1.825 is also included.

The Specification has been amended to insert the sequence listing and to add a sequence identifier number. Figure 2 of the present application has been canceled because it contains errors. Support for new Figure 2 appears in U.S.S.N. 09/641,741, filed August 18, 2000, (the '741 application). The present application claims priority to the '741 application and incorporates the '741 application by reference (*See, e.g.*, page 1 of the present application). Thus, no new matter has been added.

Additionally, Figures 14-16 misidentify sequences. The drawings have been amended to

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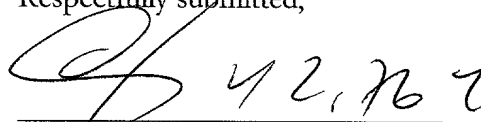
correct these informalities and to comply with the requirements of 37 C.F.R. § 1.84. No new matter has been added.

A petition for a two-month extension of time is submitted herewith. Applicants believe that no additional fee is due with the submission of this Response. However, the Commissioner is hereby authorized to charge any fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Reference No. 15966-581 CIP (Cura-81 CIP).

CONCLUSION

On the basis of the foregoing amendments and remarks, Applicants respectfully submit that the pending claims are in condition for allowance. If there are any questions regarding this submission, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,



Ivor R. Elrifi, Reg. No. 39,529

Attorney for Applicant

c/o MINTZ, LEVIN, COHN, FERRIS,
GLOVSKY & POPEO, P.C.

One Financial Center

Boston, Massachusetts 02111

Tel: (617) 542-6000

Fax: (617) 542-2241

Dated: May 8, 2002

APPENDIX A

In the Specification:

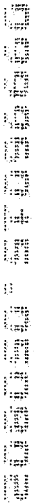
On page 6, first full paragraph:

FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO:13) and the ACPL1a polypeptide (SEQ ID) (ALO35460_GENESCAN_predicted_pep”).

TRA 1651068v1

APPENDIX B

PROPOSED AMENDMENTS TO FIGURES



Cancel

MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETAN
GTSEQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGC
PPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDA
DPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSS
GMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVS
PNDLFLEAPASGSSDPLDFQHHNYKAMRKLKQVQEQCPNITRIYSIGKSYQGLKLYVME
MSDKPGEHELGEPEORYEAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIH
LLPSMNPDGYEIAYHRGSELVGWAEGRWNNQSIDLNNFADLNTPLWEAODDGKVP
HIVPNHHLPLPTYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGEVVSYPFDMTR
TPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSODFSVHGNIINGADW
HTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKDALLTYLEQVRMGI
AGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLLTPGDYMTASAEGYHS
VTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD

Fig. 2

Insert

— — Figure 2. Protein sequence encoded by the coding sequence shown in Figure 1.

MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETA
NGTSEQHVRIKVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQET
GCPPLGLESRLRVSDSRLEASSSQSFGGLGPHRGRLNIQSGLEDGDLYDGAWCAEE
QDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGS
RNHSSGMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEIL
ACPVS DPNDLFLEAPASGSSDPLDFQH HNYKAMRKLMKQVQE QCPNITRIYSIGKSYQ
GLKLYVMEMSDKPGEHELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRG NPRV
TRLLSEMRIHLLPSMNP DGYEIA YHRGSELVGWAEGRWNNQSIDL N HNFADLNTPLW
EAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGE
LVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSODF
SVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKD
ALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLLTPG
DYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLR
RRLERLRGQKD — —

Figure 14.

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 510/510 (100%), Positives = 510/510 (100%)

Query: 1 MWGLLLAALFAPAVGPAAGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLAALFAPAVGPAAGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLAALFAPAVGPAAGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL
Sbjct: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSQSFGGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSQSFGGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSQSFGGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct: 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query: 241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct: 241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query: 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360
NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH
Sbjct: 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360

Query: 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG 420
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG
Sbjct: 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG 420

Query: 421 WAEGRWNNQSIDLNNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
WAEGRWNNQSIDLNNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
Sbjct: 421 WAEGRWNNQSIDLNNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Query: 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510 (SEQ ID NO: 45)
AVIKWMKRIPFVLSANLHGGELVVSYPFDM
Sbjct: 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510

Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 67/69 (97%), Positives = 67/69 (97%)

Query: 507 PFD-MVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR 565
P D MVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR
Sbjct: 666 PGDYMTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR 725

Query: 566 LERLRGQKD 574 (SEQ ID NO: 6) (SEQ ID NO: 46)
LERLRGQKD (SEQ ID NO: 41)
Sbjct: 726 LERLRGQKD 734 (SEQ ID NO: 42)

Figure 15

>ptnr:SP TREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101
Identities = 192/193 (99%), Positives = 193/193 (100%)

Query: 1 MWGLLLALAAFPAPVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLALAAFPAPVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLALAAFPAPVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL
Sbjct: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRD 193 [(SEQ ID NO:8)] (SEQ ID NO:47)
PTRFSGVITQGR+ (SEQ ID NO:43)
Sbjct: 181 PTRFSGVITQGRN 193 (SEQ ID NO:44)

Figure 16

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0
Identities = 734/734 (100%), Positives = 734/734 (100%)

Query: 1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Sbjct: 1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKVKIMKKRKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
Sbjct: 61 EQHVRIRVIKKKVKIMKKRKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRNLNQSGLLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRNLNQSGLLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRNSVWRYDWTYSYKVQFSNDSRTWWSRHHSSGMDAVFPANSDPETPVL 240
Sbjct: 181 PTRFSGVITQGRNSVWRYDWTYSYKVQFSNDSRTWWSRHHSSGMDAVFPANSDPETPVL 240

Query: 241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
Sbjct: 241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query: 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYMEMSDKPGHEHELGEPEVRYVAGMH 360
Sbjct: 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYMEMSDKPGHEHELGEPEVRYVAGMH 360

Query: 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG 420
Sbjct: 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG 420

Query: 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR 480
Sbjct: 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR 480

Query: 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
Sbjct: 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Query: 541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
Sbjct: 541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query: 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660
Sbjct: 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

Query: 661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTCTPKQRLRELLAAGAKVPP 720
Sbjct: 661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTCTPKQRLRELLAAGAKVPP 720

Query: 721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
DLRRRLERLRGQKD [(SEQ ID NO:45)]
Sbjct: 721 DLRRRLERLRGQKD 734 [(SEQ ID NO:46)]

APPENDIX C

SUBSTITUTE DRAWINGS

[illegible]